

EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAS	50
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN	
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS	
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN	
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLSATVQAN	
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN	
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN	
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA</u>	<u>SATV-TAVLA</u>	<u>TLL-ATVQA-</u>	

C1

	51		100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRIVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG NGENE.STGN IGWSIYYDDNH
P20	ATDTD...EDE	ELESVARSAL	VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SGELET...I SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus	-----	<u>-L--V-R--</u>	<u>V-----EG --E-E-----</u>

V1

	101		150
EG327	GVLTAGITL	KAGDNLKIKQ	NTNENTNASSFTYSLK KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSSFTYSLK KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSFTYSLK KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSFTYSLK KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNNTNENT NDSSFTYSLK KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD.....FTYSLK KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK KDLTGLINVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK KDLTGLINVE
Consensus	-----	<u>TL KAGDNLKIKQ</u>	----- <u>FTYSLK K-L--L--V-</u>
	V1	C2	V2 C3

	151		200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE TNGDPTVHLN GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H41	TEKLSFGANG	KKVNIIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDML
Consensus	<u>TEKLSF-AN-</u>	<u>-KVNII-SDTK</u>	<u>GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L</u>

C3

FIG. 1

201 250

EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVKP	GTTAS..DNV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVKP	GTTAS..DNV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN	AGWNIKGVK-	G-T-----NV

V3 C4 V4

251 300

EG327	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
H15	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
H38	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
P20	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
H41	DFVRTYDTVE	FLSADTKTTT	VNVEKDNKG	RTEVKIGAKT	SVIKEKDGKL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVEKDNKG	-TEVKIGAKT	SVIKEKDGKL

C5

301 350

EG327	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
BZ198	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
BZ10	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
H15	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
EG329	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
PMC21	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
H38	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
P20	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
Z2491	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
H41	VTGKDKGENG	SSTDKEGGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK
Consensus	VTGK-K-EN-	SSTD-GEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGOADK

C5

351 400

EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
Consensus	FETVTSGT-V	TFASG-GTTA	TVSKDDQGN	TV-YDVNVGD	ALNVNQLQNS

C5

FIG. 1 cont.

EG327	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	450
BZ198	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
BZ10	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
H15	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
EG329	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
PMC21	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
H38	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
P20	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
Z2491	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EISRNGKNID	
H41	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	
Consensus	<u>GWNLDSKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE</u>	<u>TVNINAGNNI</u>	<u>EI-RNGKNID</u>	

C5

		451				500
EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG	
BZ198	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG	
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG	
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG	
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG	
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG	
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA	LNVGSKDANK	PVRITNVAPG	
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG	
Z2491	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG	
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG	
Consensus	<u>IATSM-POFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---</u>	<u>A LNVGSK--NK</u>	<u>PVRITNVAPG</u>	

C5

		501				550
EG327	VKEGDVTNVA	QLKGVAQNIN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
BZ198	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
BZ10	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
H15	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
EG329	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
PMC21	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
H38	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
P20	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
Z2491	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
H41	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG	
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNIN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>	

C5

		551				600
EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV	
BZ198	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV	
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV	
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV	
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV	
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV	
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV	
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV	
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV	
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV	
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>	

C5

FIG. 1 cont.

601
EG327 GYQW.
BZ198 GYQW.
BZ10 GYQW.
H15 GYQW.
EG329 GYQW.
PMC21 GYQW.
H38 GYQW.
P20 GYQW.
Z2491 GYQW.
H41 GYQW.
Consensus GYQW.
C5

FIG. 1 cont.

1

H15	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	70
B210	ATGAACAAAA	TATCCCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
B2198	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
P20	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
H38	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
Z2491	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
H41	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
EG329	ATGAACGAAA	TATTGCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
PMC21	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCATGGGT	CGTCGTATCC	GAGCTCACAC	
EG327	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC	
Consensus	ATGAAC-AAA	TAT--CGCAT	CATTGGAAT	AG-GCCCTCA	ATGC-TGGGT	-G--GTATCC	GAGCTCACAC	

C1

71

H15	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	140
B210	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
B2198	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
P20	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
H38	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
Z2491	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
H41	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
EG329	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT	
PMC21	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT	
EG327	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT	
Consensus	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TG--GACCGC	CGTATTGGCG	AC-CTG-TGT	--GCAACGGT	

C1

141

H15	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	210
B210	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	
B2198	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	
P20	TCAGGCGAAT	GCTACCGATA	CCGAT.....GAAGATGAA	GAGTTAGAA	CCGTAGCAGC	CTCTGCTCTG	
H38	TCAGGCGAAT	GCTACCGATG	AAGAT.....GAAGAAGAA	GAGTTAGAA	CCGTAGTACG	CTCTGCTCTG	
Z2491	TCAGGCGAAT	GCTACCGATG	AAGAT.....GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTGCTCTG	
H41	TCAGGCGAAT	GCTACCGATG	AAGAT.....GAAGAAGAA	GAGTTAGAA	CCGTACAACG	CTCTGCTCTG	
EG329	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTGCTACG	CACCTGTTGCC	
PMC21	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CACCTGTTGCC	
EG327	TCAGGCGAGT	ACTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACCTGCTGTC	
Consensus	TCAGGC-A-T	-CTA-C-AT-	--GA-----	----GA--A	-A-TTAGA--	CCGT---ACG	C-CTG-----	

C1 V1

211

H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG	280
B210	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG	
B2198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG	
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA	
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA	
Z2491	GGG...AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGCGAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT	
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	AGCGTCAAT	TGGAAACGAT	A.....	TCATTATCAA	
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG	
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG	
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG	
Consensus	G-----	T-----	TA--GAAGC	A--G--GAA--	GAA-----	A-----	-----	

V1

FIG. 2

631
H15 AACGACAAC TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA 700
B210 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
B2198 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
P20 GGTAAACAAA GTACACATTA C.....ACT CGTGCGGCAA GTATTAAAGA TGTGTTGAAT GCGGGTTGGA
H38 AACGACAACG TTACCGATGA CAAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
Z2491 GGTAAACAAA GTACACATTA C.....ACT CGTGCGGCAA GTATTAAAGA TGTGTTGAAT GCGGGTTGGA
H41 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
EG329 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
PMC21 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
EG327 AACGACAACG TTACCGATGA CGAGAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
Consensus ----AC-A-- -TAC--AT-A C-----A-- CGTGC-GCAA G--TTAA-GA -GT-TT-AA GC-GG-TGGA

V3

C4

701
H15 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA 770
B210 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
B2198 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
P20 ATATTAAAGG TGTAAACT GGTCAACAA CTGGTCAATC AGAAATGTC GATTTCGTCC GCACCTACGA
H38 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
Z2491 ATATTAAAGG TGTAAACT GGTCAACAA CTGGTCAATC AGAAATGTC GATTTCGTCC GCACCTACGA
H41 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
EG329 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
PMC21 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
EG327 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTACGA
Consensus A-ATTAA-GG -GTTAA-C- GG--CAACA- CT-----TC -GA-AA-GT- GATTTCGTCC -GACTTACGA

C4

V4

C5

771
H15 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG 840
B210 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
B2198 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
P20 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
H38 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
Z2491 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
H41 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
EG329 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
PMC21 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
EG327 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
Consensus CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG

C5

841
H15 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA 910
B210 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
B2198 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
P20 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
H38 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
Z2491 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
H41 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
EG329 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
PMC21 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
EG327 AAAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
Consensus A-AAACCGAAG TTAATAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA

C5

911
H15 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA 980
B210 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
B2198 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
P20 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
H38 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
Z2491 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
H41 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
EG329 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
PMC21 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
EG327 AAGGCAAAG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA
Consensus AAG-CAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCCA AGGCTTAGTG ACTGCAAAG AAGTGATTGA

C5

FIG. 2 cont.

981 1050

H15	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
B210	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	TGCAGTAAAC	AAGGCTGGTT	GGAGATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG

C5

1051 1120

H15	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
B210	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
BZ198	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
P20	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
H38	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
Z2491	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
H41	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
EG329	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
PMC21	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
EG327	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA
Consensus	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTCGG	ACTGTAAGTA

C5

1121 1190

H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
B210	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT

C5

1191 1260

H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
B210	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Consensus	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT

C5

1261 1330

H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
B210	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC

C5

FIG. 2 cont.

1331
H15 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG 1400
B210 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
B2198 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
P20 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H38 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Z2491 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H41 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG329 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
PMC21 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG327 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Consensus GCAACGG-AA AAATATCGAC ATCGCCACTT CGATG-C-CC GCA-TTTTCC AGCGTTTCGC TCGG-CGCGG

C5

1401
H15 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA 1470
B210 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
B2198 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
P20 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
H38 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
Z2491 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
H41 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
EG329 GCGCGATGCG CCCACTTTAA GCGTGGAT... .GCGGACGCA TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
PMC21 GCGCGATGCG CCCACTTTAA GCGTGGAT... .GCGGACGCA TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
EG327 GCGCGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCTG GCAGCAAGGA TGCCAACAAA
Consensus GCG-GATGCG CCCACTTT-A GCGTGGAT-- --G-CGC- TTGAATGTCTG GCAGCAAG-A ---CAACAAA

C5

1471
H15 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG 1540
B210 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
B2198 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
P20 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
H38 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
Z2491 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
H41 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
EG329 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
PMC21 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
EG327 CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCGA CAACTTAAAG
Consensus CCGGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCCG- CAACTTAAAG

C5

1541
H15 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC 1610
B210 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
B2198 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
P20 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
H38 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
Z2491 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
H41 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
EG329 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
PMC21 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
EG327 GTGTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
Consensus G-GTGGCGCA AAACCTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CG-GCGG-A TCGCCCAAGC

C5

1611
H15 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT 1680
B210 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
B2198 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
P20 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
H38 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
Z2491 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
H41 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
EG329 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
PMC21 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
EG327 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
Consensus GATTGCAACC GCAGGT-T-G -TCAGGCG-TA T-TGCCCGGC AAGAGTATGA TGGCGATCGG CGGCG--ACT

C5

FIG. 2 cont.

	1681							1750
H15	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG	
BZ10	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG	
BZ198	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCAAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
P20	TATCTCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG	
H38	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
Z2491	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
H41	TATCTCGGCG	AAGCCGGTTA	TGCCATCGGC	TACTCAAGCA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
EG329	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
PMC21	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
EG327	TATCGCGGCG	AAGCCGGTTA	TGCCATCGGC	TACTCAAGCA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG	
Consensus	<u>TATC-CGGCG</u>	<u>AAGCCGGTTA</u>	<u>-GCCATCGGC</u>	<u>TACTC-AG-A</u>	<u>TTTC-G-C--</u>	<u>-GG-AATTGG</u>	<u>-TTATCAA-G</u>	

C5

	1751							1815
H15	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
BZ10	GCACGGCTTC	CGGCAATTTCG	CGCGGTCATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
BZ198	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAAT	GGTAA	
P20	GCACGGCTTC	CGGCAATTTCG	CGCGGTCATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
H38	GCACGGCTTC	CGGCAATTTCG	CGCGGTCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
Z2491	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
H41	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
EG329	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
PMC21	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
EG327	GCACGGCTTC	CGGCAATTTCG	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA	
Consensus	<u>GCACGGCTTC</u>	<u>CGGCAATTTCG</u>	<u>CGCGG-CATT</u>	<u>TCGGT-CTTC</u>	<u>CGCATCTGTC</u>	<u>GGTTATCA-T</u>	<u>GGTAA</u>	

C5

FIG. 2 cont.

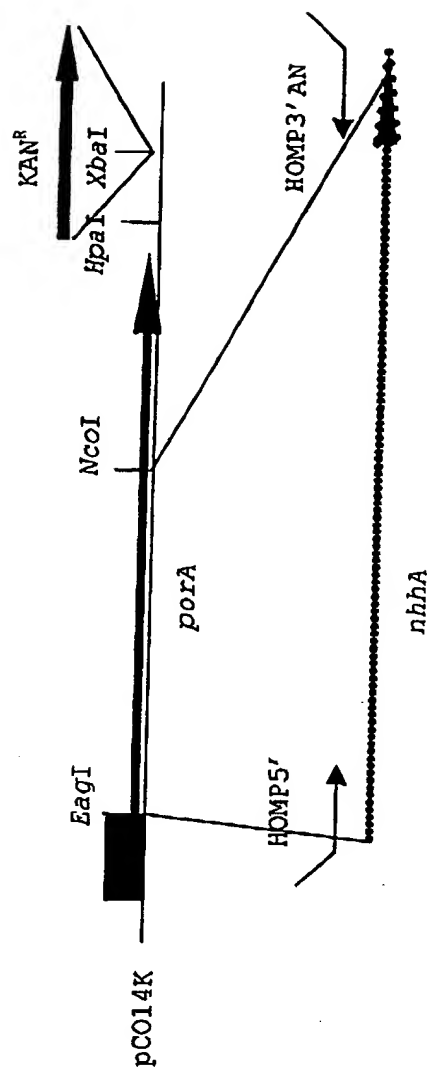


FIG. 3A

PIP52 (PMC21)

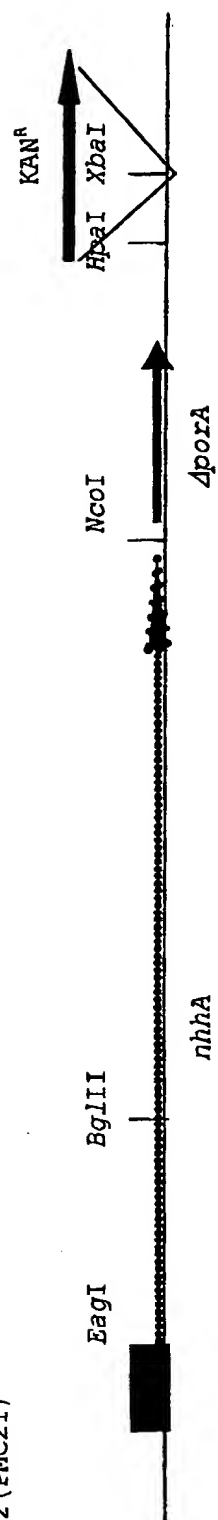


FIG. 3B

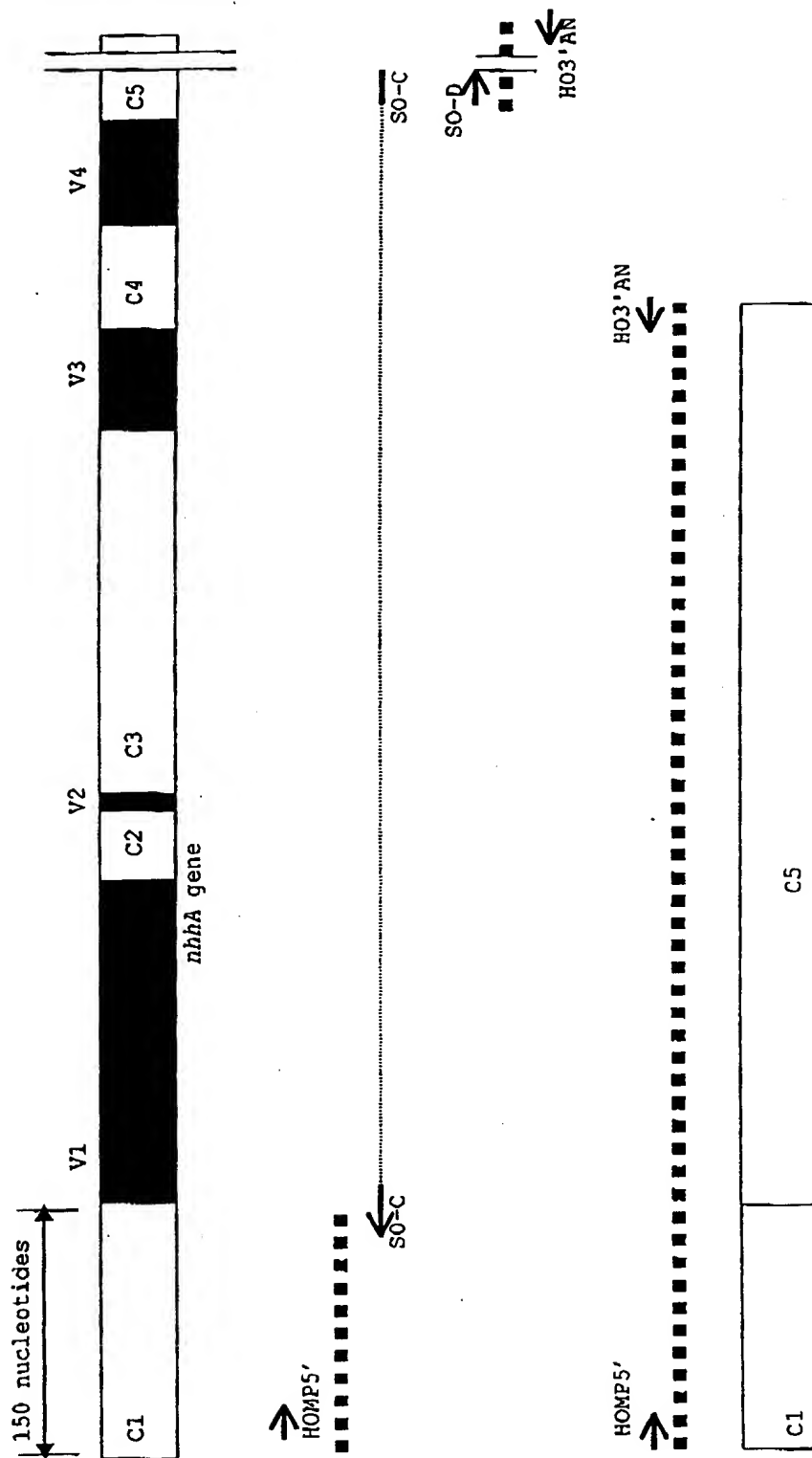


FIG. 4A

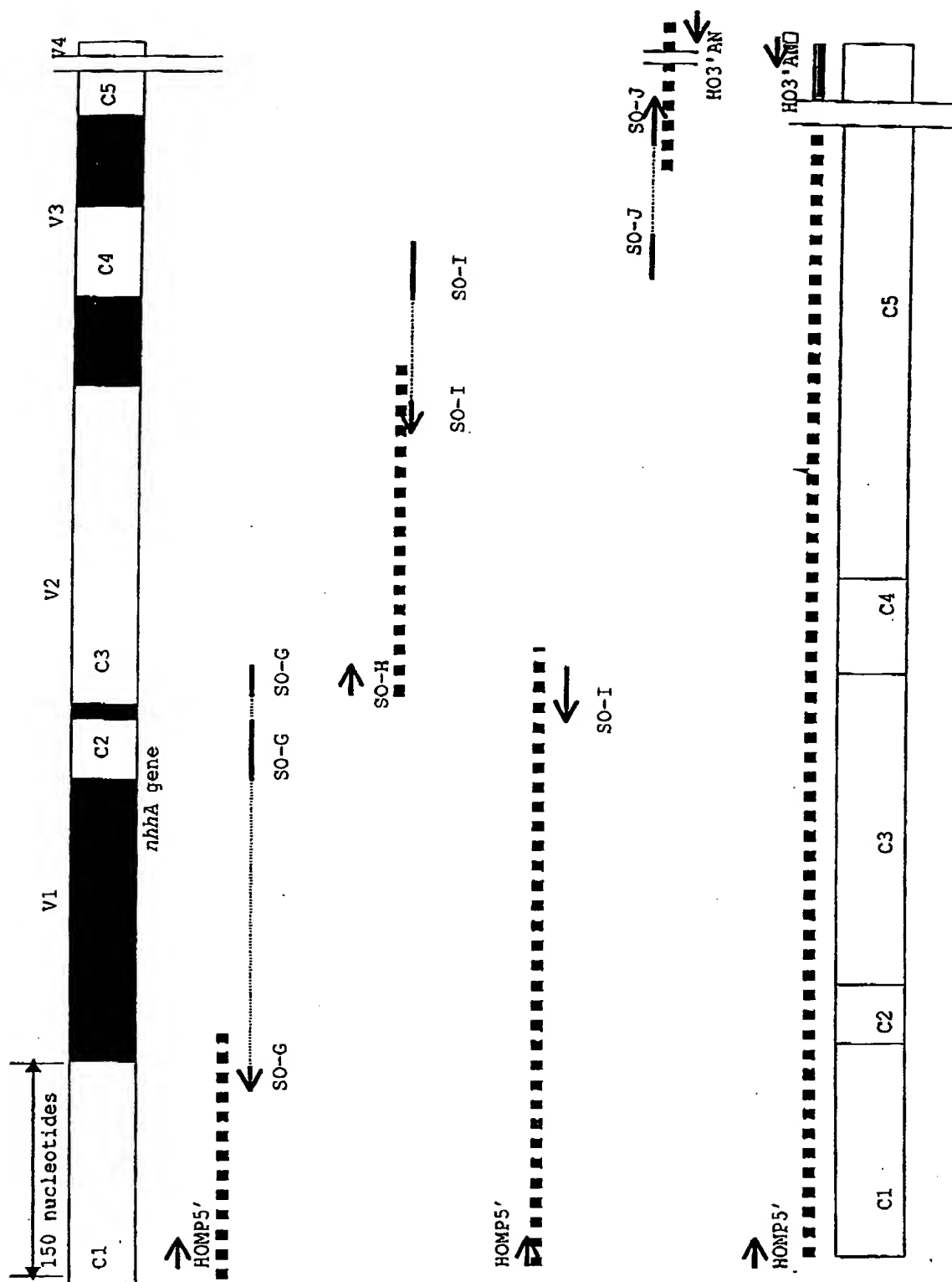


FIG. 4C

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTD LNTGATTNV TNDNVTDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNRR IDNVDGNARA GIAQAIATAG
 451 LVQAYLPKGS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCC
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAATG AAACAGATCT GACCAAGTGT GGAACGAAA AATTATCGTT
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCGTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGCGAAGG CTTAGTGACT GCAAAAGAAG
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAAACCGT
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC
 951 GGTGTCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG
 1151 TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
 1201 CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT
 1251 CGCACAACCT AAAGGCGTGG CGCAAAACCT GAACAACCGC ATCGACAATG
 1301 TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACCGCAGGT
 1351 CTGTTTCAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG
 1401 CACTTATCGC GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC
 1501 CATTCGGTG CTTCCGCATC TGTCGGTTAT CAGTGGTAA

B

FIG. 5

1 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 51 ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTDM LLNTGATTNV TNDNVTDDK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEDGDKLV TGKGKGNGS STDEGEGLVT AKEVIDAVNK AGWRMKTSTA
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGMDET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT
 51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACACGTGTGT TTGCAACGGT TCAGGCGAAT
 151 GCTACCGATG AAACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT
 201 TGGCGCAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
 251 ATTTTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CCGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAGAAG
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAAACCGT
 751 AATGGTCAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC
 951 GGTGCGAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG
 1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
 1201 GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG ATGTTACAAA
 1251 CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA
 1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
 1351 GGTCTGGTTC AGGCGTATCT GCCCGGCAAG AGTATGATGG CGATCGGCGG
 1401 CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATT
 1451 CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTCGCGC
 1501 GGCCATTTTC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

B

FIG. 6

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAFLA TLLFATVQAS
 51 ANNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
 101 DGKLVTKGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLD S KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMaIG GGTyrGEAGY AIGYSSISDG GNWIKGTAS GNSRGHFGAS
 401 ASVGyQW*

A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACACG TGTATTTCGT CCGCACTTAC GACACAGTCG AGTTCTTGAG
 201 CGCAGATACG AAAACAACGA CTGTAAATGT GGAAAGCAAA GACAACGGCA
 251 AGAAAACCGA AGTTAAAATC GGTGCGAAGA CTCTGTAT TAAAGAAAAA
 301 GACGGTAAGT TGGTACTGG TAAAGACAAA GGCGAGAAATG GTTCTTCTAC
 351 AGACGAAGGC GAAGGCTTAG TGA CTGCAA AGAAGTGATT GATGCAGTAA
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAACAGGT
 451 CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC
 501 TAGTGGTAAA GGTACAAC TGACTGTAAG TAAAGATGAT CAAGGCAACA
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG
 601 CTGCAAAACA GCGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC
 651 GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG
 701 AAACCGTCAA CATTAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
 751 AAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTTT CCAGCGTTTC
 801 GCTCGGCGCG GGGGCGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT
 851 TGAATGTCGG CAGCAAGAAG GACAACAAC CCGTCCGCAT TACCAATGTC
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
 951 CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC
 1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT
 1051 TTGCCCCGCA AGAGTATGAT GGCATCGGC GCGGCGACTT ATCGCGGCGA
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA
 1151 TTATCAAAGG CACGGCTTCC GGCAATTCGC GCGGCCATTT CCGTGCTTCC
 1201 GCATCTGTCT GTTATCAGTG GTAA

B

FIG. 7

1 MNKIYRIIW SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNL TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
 251 VSFSKGMDE TVNINAGNNI EITRNGKNID IATSMTPOFS SVSLGAGADA
 301 PTLSDVDGAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLLN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKG TASGNSR GHFGASASVG YQW*

A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT
 201 TAAAGGCGTT AAACCCGGTA CAACAGCTTC CGATAACGTT GATTTCGTCC
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACCAAGACT
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAATCGG
 351 TGC GAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 401 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACCAAGGCGA AGGCTTAGTG
 451 ACTGCAAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA
 501 AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACGCG
 601 ACTGTAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA
 651 TGTGCGCGAT GCCCTAAACG TCAATCAGCT GCAAAACAGC GGTGGAATT
 701 TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG
 801 CAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT
 851 CGATGACCCC GCAGTTTCC AGCGTTTCGC TCGGCGCGGG GCGGATGCG
 901 CCCACTTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG
 1001 ATGTTACAAA CGTCGCACAA CTAAAGGCG TGGCGCAAAA CTTGAACAAC
 1051 CGCATCGACA ATGTGGACGG CAACGCGCGT GCGGGCATCG CCAAGCGAT
 1101 TGCAACCGCA GGTCTGGTTC AGGCGTATTT GCGCGCAAG AGTATGATGG
 1151 CGATCGGCGG CCGCACTTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC
 1201 TCCAGTATTT CCGACGGCGG AAATGCGATT ATCAAAGGCA CGGCTTCCGG
 1251 CAATTCGCGC GGCCATTTCC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT
 1301 AA

B

FIG. 8

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
 101 GLNFAKETAG TNGDITVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTTV NVEKDNKGKK TEVKIGAKTS VIKEDGKLV
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKF
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
 301 WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTINVAQL KGVAQNLNLR IDNVNENARA GIAQAIATAG LVQAYLPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
 501 QW*

A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTCACCTA
 201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT
 251 TATCGTTTAG CGCAAACGGC AATAAAGTCA ACATCACAAAG CGACACCAAA
 301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 351 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATCGTGCG GCAAGCGTTA
 401 AAGACGTATT AAACGCTGGC TGGAAACATTA AAGGCGTTAA AAACGTTGAT
 451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC
 501 AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA
 551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT
 601 ACTGGTAAAG ACAAGGCGA GAATGTTTCT TCTACAGACG AAGGCGAAGG
 651 CTTAGTGAAT GCAAAAGAAG TGATTGATGC AGTAAACAAG GCTGGTTGGA
 701 GAATGAAAAC AACAACCGCT AATGGTCAAA CAGGTCAAGC TGACAAGTTT
 751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC
 801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG
 851 ATGTAAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT
 901 TGGAAATTTG ATTCCAAAGC GGTTCGAGGT TCTTCGGGCA AAGTCATCAG
 951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA
 1001 ATGCCCGCAA CAACATCGAG ATTACCCGCA ACGGTAAAAA TATCGACATC
 1051 GCCACTTCGA TGACCCCGCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC
 1101 GGATGCGCCC ACTTTGAGCG TGGATGGGGA CGCATTGAAT GTCGGCAGCA
 1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAAA
 1201 GAGGGGGGATG TTACAAACGT CGCACAACTT AAAGGCGTGG CGCAAACTT
 1251 GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGCG GGCATCGCCC
 1301 AAGCGATTGC AACCAGAGGT CTGGTTCAGG CGTATTTGCC CGGCAAGAGT
 1351 ATGATGGCGA TCGGCGGCGG CACTTATCGC GCGGAAGCCG GTTACGCCAT
 1401 CGGCTACTCC AGTATTTCCG ACGGCGGAAA TTGGATTATC AAAGGCACGG
 1451 CTTCCGGCAA TTCGCGCGGC CATTTCCGGT CTTCCGCATC TGTCGGTTAT
 1501 CAGTGGTAA

B

FIG. 9

1 50

H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN

PMC21 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN

PMC21Bgldel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

PMC21C1C5 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

C1

51 100

H41 ATDED...EEE ELESVQRS.V VGSIOASMEG SVELET...I SLSMTNDSKE

PMC21 ANNEEQEYYL YLHPVORTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK

H41Studel ATDE.....

PMC21Bgldel ANNE.....

PMC21C1C5 AN.....

V1

101 150

H41 FVDPYIVVTI KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK

PMC21 GVLTAIREITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK

H41StudelTGLINVETEK

PMC21BgldelTDLTSVGTEK

PMC21C1C5

V1 C2 V2 C3

151 200

H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT

PMC21 LSFSAHGKLV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT

H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT

PMC21Bgldel LSFSANGKLV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTOTLLNT

PMC21C1C5

C3 V3

201 250

H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21Bgldel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21C1C5NVDFVRT

V3 C4 V4 C5

251 300

H41 YDTVEFLSAD TKTTTVNVES KONGKKTEVK IGAKTSVIKE KDGKLVGTGK

PMC21 YDTVEFLSAD TKTTTVNVES KONGKKTEVK IGAKTSVIKE KDGKLVGTGK

H41Studel YDTVEFLSAD TKTTTVNVES KONGKKTEVK IGAKTSVIKE KDGKLVGTGK

PMC21Bgldel YDTVEFLSAD TKTTTVNVES KONGKKTEVK IGAKTSVIKE KDGKLVGTGK

PMC21C1C5 YDTVEFLSAD TKTTTVNVES KONGKKTEVK IGAKTSVIKE KDGKLVGTGK

C5

301 350

H41 KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT GOADKFETVT

PMC21 KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT GOADKFETVT

H41Studel KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT GOADKFETVT

PMC21Bgldel KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT GOADKFETVT

PMC21C1C5 KGENGSSIDE GEGLVTAKEV IDAVNKAGWR MKTTTANGOT GOADKFETVT

C5

351 400

H41 SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD

PMC21 SGTNVTFASG KGTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD

H41Studel SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD

PMC21Bgldel SGTNVTFASG KGTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD

PMC21C1C5 SGTNVTFASG KGTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD

C5

FIG. 10

401 450
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
C5

451 500
H41 TPQFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVRI NVAPGVKEGD
PMC21 TPQFSSVSLG AGADAPTLV DG.DALNVGS KKDNKPVRI NVAPGVKEGD
H41Studel TPQFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVRI NVAPGVKEGD
PMC21Bgldel TPQFSSVSLG AGADAPTLV DG.DALNVGS KKDNKPVRI NVAPGVKEGD
PMC21C1C5 TPQFSSVSLG AGADAPTLV DG.DALNVGS KKDNKPVRI NVAPGVKEGD
C5

501 550
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA
C5

551 600
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
C5

FIG. 10 cont'd

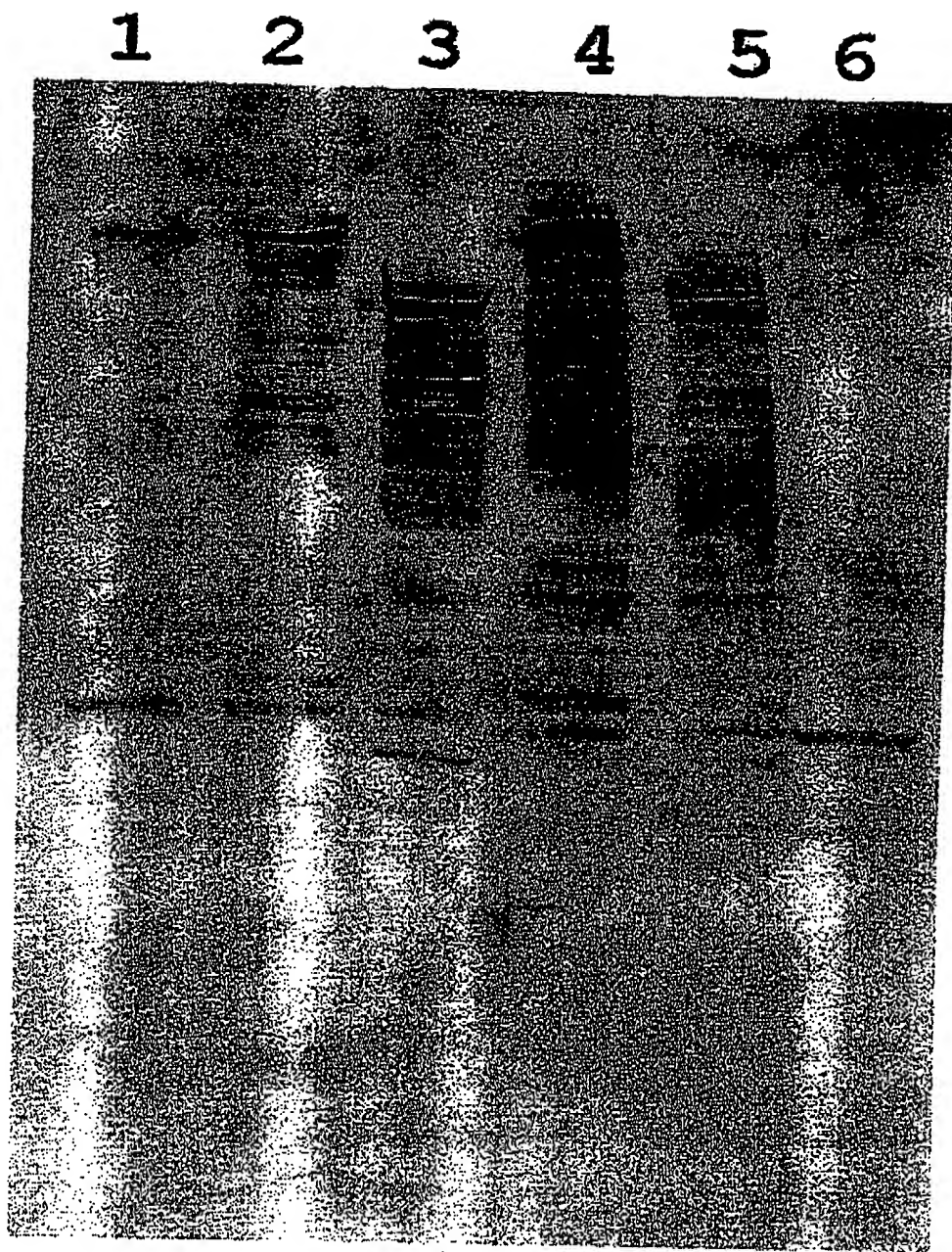


FIG. 11

1 2 3 4 5 6 7

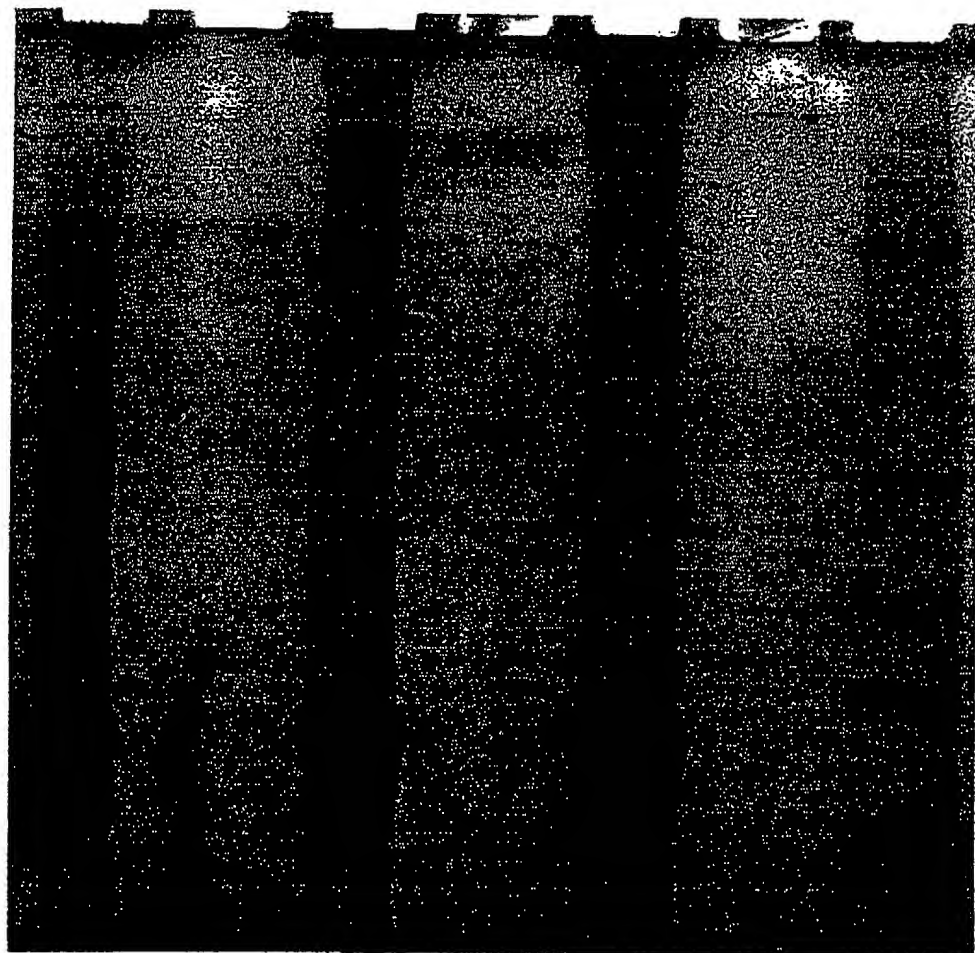
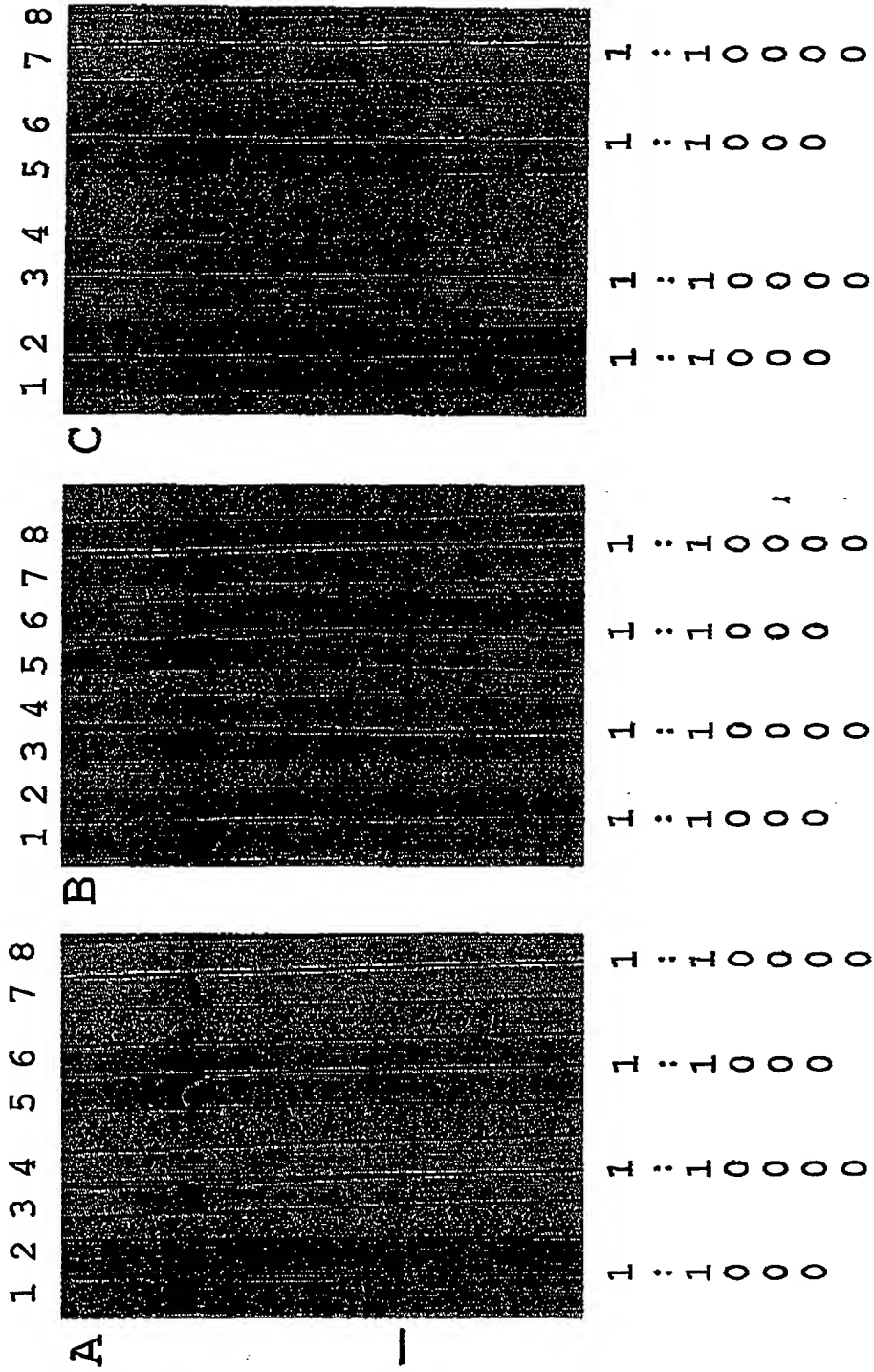


FIG. 12



173—

FIG. 13

A

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
101 GVLTAAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
151 NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT
201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF
351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401 SGKVISGNVS PSKKGMDTV NINAGNNIEI TRNGKNIDIA TSMTQPQSSV
451 SLGAGADAPT LSVGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
501 GVAQNLLNRI DNVGDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
551 EAGYAIGYSS ISDGGNWIIG GTASGNSRGH FGASASVGYQ W*

B

52 TDEDEEEEL ESQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI
101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG
151 KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT
201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTKVTF
351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401 SGKVISGNVS PSKKGMDTV NINAGNNIEI TRNGKNIDIA TSMTQPQSSV
451 SLGAGADAPT LSVDDGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL
501 KGVAQNLLNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVGY QW*

FIG. 14

C

52 NNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLTDT LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKG VK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNV DGNARA GIAQAIATAG
451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
501 HFGASASVGY QW*

D

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLTDM LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKG VK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501 GHFGASASVG YQW*

FIG. 14

E

52 NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIEKEK
 101 DGKLVTGKDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
 301 APGVKEGDTV NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMMAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
 401 ASVGYQW*

F

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIEKEDGKL VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTH ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
 251 VSPSKGKMD E TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
 301 PTLSDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLLN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

G

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITS DTK
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIEKEDGKLV
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTHA NGQTGQADKF
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
 301 WNLDKAVAG SSGKVISGNV SPSKGKMD E TVNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTNVAQL KGVAQNLLNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVG
 501 QW*

FIG. 14